

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

Atty. Docket No.: 2551-026

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Douglas M. BLAIR

Appln. No.: 09/881,234

Group Art Unit: 1631

Filing Date: June 14, 2001

Examiner: Smith, C.

TECH CENTER 1600/2900

For: APPARATUS AND METHOD FOR PROVIDING SEQUENCE DATABASE
COMPARISON

Commissioner for Patents
Washington, D.C. 20231

#31A

Plunkett

12/4/02

OFFICE ACTION ELECTION / RESPONSE

Sir:

Applicant respectfully requests entry of the following amendment and
reconsideration based on the accompanying remarks.

In the Drawings:

Please replace the drawing sheets containing **figures 2A** and **6** with the attached
replacement drawing sheets.

In the Specification:

Please replace paragraph 56 as follows:

A
"Figures 2A-C illustrate the relationship of the data element of the present
invention to the database sequences."

Please replace paragraph 80 as follows:

A2
"Figures 2A-B illustrate the relationship of the data element of the present

*PL
curr*

invention to the database sequences. **Figure 2A** shows one of the two (query or subject) databases **20** composed of some number of sequences having boundaries **22**, as illustrated in enlarged view **Figure 2C**. These sequences are grouped into sets of sequences, each set comprising a data element **24**. Data elements are of approximately a user-defined desired data size. If the user chooses that no sequences will be split between data elements, each sequence is placed in its entirety into one data element and the data elements do not overlap, as illustrated at **23**. If the user chooses otherwise, as in individual sequences may be "split" between data elements, with a redundant portion of the sequence, or overlap **26**, being placed in two data elements, as illustrated by the overlapping data elements at **25**."

REMARKS

Claims 1-23 remain in the application. The drawing sheet containing **figure 2A** was replaced so as to label the enlarged view as **figure 2C**. The drawing sheet containing **figure 6** was replaced to correct the top margin. The specification was amended so as to properly refer to the enlarged view labeled **figure 2C**. No new matter has been added.

Drawing Objections

As noted above, new drawing sheets have been filed herewith to address the drawing objections noted on PTO Form 948.

Election/Restriction

The Office Action includes a requirement for an election of species.

Applicant hereby traverses the election requirement as being improper under M.P.E.P. 803.02, which clearly states:

"If the members of the Markush group are **sufficiently few in number or** so closely related that a search and examination of the entire claim can be made without serious burden, the examiner must examine all claims on the merits, even though they are directed to independent and distinct inventions. In such a case, the examiner will not follow the procedure described below and will not require restriction.

Since the decisions in *In re Weber*, 580 F.2d 455, 198 USPQ 328 (CCPA 1978) and *In re Haas*, 580 F.2d 461, 198 USPQ 334 (CCPA 1978), it is **improper for the Office to refuse to examine** that which applicants regard as their invention, **unless the subject matter in a claim lacks unity of invention**. *In re Harnish*, 631 F.2d 716, 206 USPQ 300 (CCPA 1980); and *Ex parte Hozumi*, 3 USPQ2d 1059 (Bd. Pat. App. & Int. 1984). Broadly, unity of invention exists where compounds included within a Markush group (1) share a common utility, and (2) share a substantial structural feature disclosed as being essential to that utility." (*emphasis added*)

The basis of the present election requirement appears to be the Markush-type claims 12 and 23, wherein Specie A relates to "polynucleotide" data elements or datasets selected from genomic databases and Specie B relates to "polypeptide" data elements or datasets selected from proteomic databases:

12. The method of claim [c1] wherein said datasets are selected from the group consisting of genomic and proteomic databases.
23. The system of claim [c13], wherein said datasets are selected from the group consisting of genomic and proteomic databases.

In the present case, even though the Markush group claims independent and distinct inventions, it has the fewest number of members possible, two, which is "sufficiently few in number" so as to "not require restriction" under M.P.E.P. 803.02.

Additionally, Applicant respectfully submits that unity of invention exists because polynucleotides and polypeptides (1) share a common utility as informational biomolecules and (2) share a substantial structural feature of linear polymeric molecules

made up of sequences of individual units, such that it is improper for the Office to refuse to examine that which Applicant regards as his invention.

However, in order to comply 35 USC 121, Applicant hereby elects **specie A**, **claims 1-23**, for prosecution on the merits if the guidance of M.P.E.P. 803.02 is to be ignored.

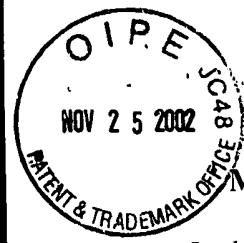
Conclusion

For the reasons stated above, Applicants submit that the application and claims 1-23 are ready for examination on the merits. If there remain any issues that may be disposed of via a telephonic interview, the Examiner is kindly invited to contact the undersigned at the local exchange given below.

Respectfully,



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MARKED-UP VERSION SHOWING CHANGES MADE BY AMENDMENT

In the Drawings:

Drawing sheets containing **figures 2A** and **6** were replaced with the attached replacement drawing sheets, with the enlarged view of **figure 2A** being labeled as **figure 2C** and the top margin being corrected in **figure 6**.

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In the Specification:

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Paragraph 56 was amended as follows:

"**Figures 2A-[B]C** illustrate the relationship of the data element of the present invention to the database sequences."

Paragraph 80 was amended as follows:

"**Figures 2A-B** illustrate the relationship of the data element of the present invention to the database sequences. **Figure 2A** shows one of the two (query or subject) databases **20** composed of some number of sequences having boundaries **22**, as illustrated in enlarged view **Figure 2C**. These sequences are grouped into sets of sequences, each set comprising a data element **24**. Data elements are of approximately a user-defined desired data size. If the user chooses that no sequences will be split between data elements, each sequence is placed in its entirety into one data element and the data elements do not overlap, as illustrated at **23**. If the user chooses otherwise, as in individual sequences may be "split" between data elements, with a redundant portion of the sequence, or overlap **26**, being placed in two data elements, as illustrated by the overlapping data elements at **25**."